                        SEQUENCE LISTING

<110>   MADDON, Paul J.

        DONOVAN, Gerald P.

        OLSON, William C.

        SCHÜLKE, Norbert

        GARDNER, Jason

        MA, Dangshe

Please remove all above foreign accent marks--they are non-ASCII
characters and cannot be processed.

<210>   14

<211>   481

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   Includes BamHI/Bg1II cloning junction, signal peptide, V region,
portion of C region and 3'XbaI/NheI (heavy) or NheI (light) cloning
junction

The above <223> response exceeds 72 characters per line; per 1.823 of
the Sequence Rules, a maximum of 72 characters per line, including white
spaces. This line-length problem appears in subsequent sequences, too.
****

Validated By CRFValidator v 1.0.3

Application No: 10695667   Version No: 2.0

Input Set:

Output Set:

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          Started:  2007-08-27 11:46:11.987
         Finished:  2007-08-27 11:46:18.117
          Elapsed:  0 hr(s) 0 min(s) 6 sec(s) 130 ms
   Total Warnings:  26
     Total Errors:  0
No. of SeqIDs Defined:  37
  Actual SeqID Count:  37
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Error code   Error Description

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W   213        Artificial or Unknown found in <213>  in SEQ ID (2)

W   213        Artificial or Unknown found in <213>  in SEQ ID (3)

W   213        Artificial or Unknown found in <213>  in SEQ ID (4)

W   213        Artificial or Unknown found in <213>  in SEQ ID (5)

W   213        Artificial or Unknown found in <213>  in SEQ ID (6)

W   213        Artificial or Unknown found in <213>  in SEQ ID (7)

W   213        Artificial or Unknown found in <213>  in SEQ ID (8)

W   213        Artificial or Unknown found in <213>  in SEQ ID (9)

W   213        Artificial or Unknown found in <213>  in SEQ ID (10)

W   213        Artificial or Unknown found in <213>  in SEQ ID (11)

W   213        Artificial or Unknown found in <213>  in SEQ ID (12)

W   213        Artificial or Unknown found in <213>  in SEQ ID (13)

W   213        Artificial or Unknown found in <213>  in SEQ ID (14)

W   213        Artificial or Unknown found in <213>  in SEQ ID (16)

W   213        Artificial or Unknown found in <213>  in SEQ ID (18)

W   213        Artificial or Unknown found in <213>  in SEQ ID (20)

W   213        Artificial or Unknown found in <213>  in SEQ ID (22)

W   213        Artificial or Unknown found in <213>  in SEQ ID (24)

W   213        Artificial or Unknown found in <213>  in SEQ ID (26)

W   213        Artificial or Unknown found in <213>  in SEQ ID (28)
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Input Set:

          Output Set:

          Started: 2007-08-27 11:46:11.987
         Finished: 2007-08-27 11:46:18.117
          Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 130 ms
   Total Warnings: 26
     Total Errors: 0
No. of SeqIDs Defined: 37
  Actual SeqID Count: 37

Error code   Error Description

          This error has occured more than 20 times, will not be displayed

<210> 1

<211> 750

<212> PRT

<213> Homo sapiens

<400> 1

Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
1   5   10   15

Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
            20   25   30

Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
        35   40   45

Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
        50   55   60

Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
65   70   75   80

Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
            85   90   95

Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
            100   105   110

Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
            115   120   125

Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
        130   135   140

Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
145   150   155   160

Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
            165   170   175

Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met

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                180                     185                     190


Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
        195                     200                     205


Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
        210                     215                     220


Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
225                     230                     235                     240


Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
                245                     250                     255


Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
                260                     265                     270


Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
        275                     280                     285


Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys
        290                     295                     300


Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg
305                     310                     315                     320


Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
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Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
                340                     345                     350


Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
        355                     360                     365


Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
        370                     375                     380


Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg
385                     390                     395                     400


Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
                405                     410                     415
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Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
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Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
        435   440   445

Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
    450   455   460

Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
465   470   475   480

Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser
                485   490   495

Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile
            500   505   510

Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu
        515   520   525

Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn
    530   535   540

Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu
545   550   555   560

Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val
                565   570   575

Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
                580   585   590

Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
        595   600   605

Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
        610   615   620

Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
625   630   635   640

Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
              645   650   655

Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
              660   665   670

Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
              675   680   685

His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
           690   695   700

Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
705   710   715   720

Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
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Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
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<211> 7570

<212> DNA

<213> Artificial Sequence

<220>

<223> Plasmid

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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc   180

ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt   240

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tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc   360

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<211> 7597

<212> DNA

<213> Artificial Sequence

<220>

<223> Plasmid

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